Blast 2 S qu nc s results

| PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure |

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix [BLOSUM62 ↕] gap open: [11] gap extension: [1]
x_dropoff: [50] expect: [10.00] wordsize: [3] Filter   [Align]

Sequence 1 gi 3702836 hASIC3 [Homo sapiens] Length 531
Sequence 2 gi 13592019 P2X3 [Rattus norvegicus] Length 397
N significant similarity was found

Align two sequences

Tue Apr 15 17:04:02 BST 2003

```
/usr/tmp/seq1.214485.sca :   397 aa
>gi|13592019|ref|NP_112337.1| P2X3   [Rattus norve    397 aa vs.
>gi|3702836|gb|AAC62935.1| hASIC3 [Homo sapiens],    531 aa
scoring matrix: , gap penalties: ~12/~2
15.7% identity;  Global alignment score: ~167
```

```
                  10            20            30          40
/usr/t MNCIS---------DFFTYETTKSV-----VVKSWTI----GIINRAVQLLIISYFVGW
       :.  :          :.  ..  .. :.      :     ..     :.   :: :  ...
gi|370 MKPTSGPEEARRQPSDIRVFASNCSMHGLGHVFGPGSLSLRRGMWAAAVVLSVATFLYQV
            10           20            30          40         50          60


                50            60                70
/usr/t V---------FLHEKAYQVRDT---AIESSVVTKVKGFGR----------YANRVM---DVS
       .          : :. :  .  :..     ..  ..  ...  .:        .:.  ..   :  .
gi|370 AERVRYYREFHHQTALDERESHRLVFPAVTLCNINPLRRSRLTPNDLHWAGSALLGLDPA
            70           80          90           100        110         120


  80                  90         100         110      120          130
/usr/t DYVT-------PPQGTSVFVIITKIIVTENQMQGFCPENEEKYRCVSDSQ-CGPERFPGG
       ....          ::      .  :.    .  ...   ..      ..    :    .: :!::: :
gi|370 EHAAFLRALGRPPAPPG-FMPSPTFDMAQLYARAGHSLDDMLLDCRFRGQPCGPENFTTI
            130          140          150         160        170


                140                   150
/usr/t GILTGRCVNYSS------VLRTC------------EIQG------W-----CPTEVD---
       :..:  ...:        .: :              ..:        :           : ::
gi|370 FTRMGKCYTFNSGADGAELLTTTRGGMGNGLDIMLDVQQEEYLPVWRDNEETPFEVGIRV
         180          190          200         210        220         230


            160           170          180         190         200
/usr/t ---TVEMPIMME------AENFTIFI---KNSIRF---PLFNFEKGNLLPNLTDKDIKRC
       . : :  ...         . .. :.     .... :    :   ...: ::     . .:
gi|370 QIHSQEEPPIIDQLGLGVSPGYQTFVSCQQQQLSFLPPPWGDCSSASLNPNY-EPEPSDP
         240          250          260         270        280         290


            210        220         230         240         250          260
/usr/t RFHPEKAPFCPILRVGDVVKFAGQDFAKLARTGGVLGIKIGW---VCDLDKAWDQCIPKY
       : .:  :  . ,.: .      .:: .        ::. . . .:
gi|370 LGSPSPSPSPPYTLMG--CRLACET-RYVARKCGCRMVYMPGDVPVCS-PQQYKNC----
         300         310          320         330         340         350


            270        280         290                      300
/usr/t SFTRLDGVSEKSSVS---PGYNFRFAKYYKM---ENGSEYRTLLK-------------A
       .    .:.. .:.: .     :    . :.:!   .:     . ,   : :  .         :
gi|370 AHPAIDAILRKDSCACPNPCASTRYAKELSMVRIPSRAAARFLARKLNRSEAYIAENVLA
            360          370          380         390         400         410
```

```
              310            320        330              340
/usr/t FGIRPDVLVYGNAGK------FNIIPTIISSVAAFTSVGVGTVL------CDII---LLN
       . : :..: : .. .      ... : .... : .... :.:    :...   .:.
gi|370 LDIFFEALNYETVEQKKAYEMSELLGDIGGQMGLFIGASLLTILEILDYLCEVFRDKVLG
              420       430       440       450       460       470


              350       360       370            380        390
/usr/t FLKGADHYKARKFEEVTETTLKGTASTN--------PVFASDQATVEKQSTDSG--AYSIG
       .. . .: . .. .. . : :. :.      ;  .  .: :  . :    : .
gi|370 YFWNRQHSQRHSSTNLLQEGL-GSHRTQVPHLSLGPRPPTPPCAVTKTLSASHRTCYLVT
              480       490       500       510       520


/usr/t H-

gi|370 QL
       530

Elapsed time:   0:00:00
```

Blast 2 Sequ nces results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix [BLOSUM62 ⬍] gap open:[11] gap extension: [1]
x_dropoff: [50] expect:[10.00]wordsize: [3] Filter   [Align]

Sequence 1 gi 3702836   proton-gated cation channel subunit [Homo sapiens]   **Length 531**
Sequence 2 gi 12643353 P2X purinoceptor 2 (ATP receptor) (P2X2) (Purinergic receptor) **Length 471**
No significant similarity was found

Sequence Alignment Output

Align two sequences

Tue Apr 15 18:49:23 BST 2003

```
/usr/tmp/seq1.215975.sca :   472 aa
>gi|1352688|sp|P49653|P2X2_RAT P2X purinoceptor 2    472 aa vs.
>gi|3702836|gb|AAC62935.1| hASIC3 [Homo sapiens],   531 aa
scoring matrix: , gap penalties: -12/-2
17.1% identity;  Global alignment score: -108

                     10        20        30        40
/usr/t  M---------------VRRLARGC-WSAFWDYETPKVIVVRNRRLGFVHRMVQLLILLYF
        :          .: .: .:     ..      :   . .: :  .   .... .::
gi|370  MKPTSGPEEARRQPSDIRVFASNCSMHGLGHVFGPGSLSLR-RGMWAAAVVLSVATFLYQ
            10        20        30        40        50

                50        60           70        80
/usr/t  V------WYVFIVQKSYQDSETG----PESSI--ITKVKGITMSEDKV-WDVEEYV--KP
        :       .  :  :  .. :.      :   ..   ..  .. :    .  .   :
gi|370  VAERVRYYREFBHQTALDERESHRLVFPAVTLCNINPLRRSRLTPNDLHWAGSALLGLDP
        60        70        80        90        100       110

        90        100       110       120       130       140
/usr/t  PEGGSVVSIITRIEVTPSQTLGTCPESMRVHSSTCHSDDDCIAGQLDMQGNGIRTGHCVP
        :  \..   .: . :.       :.   . ....  . :: :: .   ::  .  .: : :
gi|370  AEHAAFLRALGRPPAPPGFMPSPTFDMAQLYARAGHSLDDML---LDCR---FRGQPCGP
        120       130       140       150       160       170

        150       160       170       180       190       200
/usr/t  YYHGDSKTCEVSAWCPVEDGTSDNHFL-----GKMAPNFTIL--IKNSIHYPKFKFSKGN
           .         . :  .. . .: :    :  : :. .. !.    ...  . : .     :
gi|370  ENF--TTIFTRMGKCYTFNSGADGAELLTTTRGGMGNGLDIMLDVQQEEYLPVWR---DN
            180       190       200       210       220

        210       220       230       240       250       260
/usr/t  IASQKSDYLKHCTFDQDSDPYCPIFRLGFIVEKAGENFTELAHKGGVIGVIINWNCDLDL
             ..     .:.  :    :  .::. :   . ..:.    ..   .  .  :.   :
gi|370  EETPFEVGIRVQIRSQEEPPI--IDQLGLGVSPGYQTFVSCQQQQLSF-LPPPWG---DC
        230       240       250       260       270       280

        270       280       290       300       310
/usr/t  SESECNPKYSFRRLDPKYDPASSGYNFRFAKYYKING---TTTTRTLIKAYGIRIDVIVH
        : .  ::.:   .  ::   .:. :     . : .:     ::  . : :. : .
gi|370  SSASLNPNYEPEPSDPLGSPSPSP-----SPPYTLMGCRLACETRYVARKCGCRM-VYMP
            290       300       310       320       330

        320       330       340       350       360       370
/usr/t  GQAGKFSLIPTIINLATALTSI-GVGSFLCDWILLTFMNKNKLYSHKKFDKVRTPKHPSS
        :..     :    :. .:     :   . :      :. :.... :: :... ..
gi|370  GDVPVCSPQQYKNCAHPAIDAILRKDSCACPNPCASTR-----YA-KELSMVRIPSRAAA
            340       350       360       370           380       390
```

Sequence Alignment Output

```
          380                 390        400        410                 420
/usr/t RW--------PVTLA---LVLGQIPPPPSHYSQDQPPSPPSGE-----GPTLGE--GAEL
       :.           . .:   :.:  .    .. . .:  .     .:     :  .:    :: :
gi|370 RFLARKLNRSEAYIAENVLALDIFFEALNYETVEQKKAYEMSELLGDIGGQMGLFIGASL
          400        410        420        430        440         450


          430                            440                  450
/usr/t PLAVQS-PRPCSI-------------------SALTEQVVDTLGQH-------MGQRPPVP
        ..         : .              . :.  .  . ::.:      .: :::.:
gi|370 LTILEILDYLCEVFRDKVLGYFWNRQHSQRHSSTNLLQEGLGSHRTQVPHLSLGPRPPTP
          460        470        480        490        500         510


          460        470
/usr/t EPSQQDSTSTDPKG---LAQL
        .     . :.. .    ..::
gi|370 PCAVTKTLSASHRTCYLVTQL
          520        530


Elapsed time:  0:00:00
```